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(54) Title: HIV PEPTIDES, ANTIGENS, VACCINE COMPOSITIONS, IMMUNOASSAY KIT AND A METHOD OF DETECTING ANTIBODIES INDUCED BY HIV

(57) Abstract: The present invention comprises novel and modified peptides capable of inducing a HIV-1 specific immune response without antagonizing the cytotoxic T-cell activity in order to achieve an effective prophylactic and therapeutic vaccine against HIV. The peptides are based on conserved regions of HIV gag p17 and p24 proteins. Antigens in free- or carrier-bound form comprising at least one of the said peptides, vaccine compositions containing at least one of the antigens, immunoassay kits and a method of detecting antibodies induced by HIV or HIV specific peptides using such antigens, are described.

Title : HIV peptides, antigens, vaccine compositions, immunoassay kit and a method of detecting antibodies induc d by HIV

The present invention relates to novel peptides based on conserved regions of HIV gag p17 and p24, antigens in free or carrier-bound form comprising at least one of the said peptides, vaccine compositions containing at least one of the antigens, immunoassay kits and a method of detecting antibodies, induced by human immunodeficiency virus (HIV) or HIV-specific peptides, using such antigens.

BACKGROUND

There is an urgent need to control the global epidemic of HIV infection and the development of a vaccine against HIV is one of the major objectives in AIDS research. In general vaccines should activate antigen presenting cells, overcome genetic restriction in T-cell responses and generate T- and B-memory cells. The variability of the viral population poses a further difficulty in obtaining an effective HIV vaccine. A break through in the ongoing attempts to develop a vaccine against AIDS has so far not been reported. It is now generally accepted that an induction of antigen-specific humoral and cell-mediated immunity is crucial for a development of an effective prophylactic and therapeutic vaccine. All three arms of the immune system including neutralizing antibodies; CD8+CTL and T-helper-1 (TH1) cells might be required for protective immunity to HIV. It is known that CTL can clear other viral infections (Ada, Immunol. Cell Biol., 72:447-454, 1994) and that CTL can lyse infected targets early in infection before viral progeny can be produced and released by cell lysis, Ada et al., *supra*. The focus has been on selection of antigens as well as on design and evaluation of different adjuvances. The antigens used in different *in vitro* and *in vivo* studies have been all from crude proteins to various synthetic peptides from several of the HIV proteins. A large number of studies have been done on the V3 loop of gp120. Induction of both B- and T-cell responses have been observed, however, it has been reported from an in vitro study that a peptide from the conserved region of gp41 have indicated infection enhancement (Bell S.J., et al., Clin. Exp. Immunol., 87 (1) : 37-45, (January 1992).

Naturally occurring HIV sequences in vaccine candidates are not capable of stimulating a stable immune response due to the viruses inherent ability to hide by changing the appearance of the epitopes presented on the cell surface of infected cells. The immune

system is fooled to believe that a particular amino acid sequence is relevant when in fact the amino acids of importance is hidden.

A recent study of titers of antibodies against the gag p24 protein, has shown that slow progression towards development of AIDS is associated with high titers, while fast progression towards development of AIDS is associated with low titers. It is shown that persons with low p24 antibody titer develop significantly faster AIDS than persons with high p24 antibody titers (Zwart G., et al. Virology, 201, p. 285-93, June 1994), indicating that gag and p24 in particular can play a key role to control the development of AIDS.

New HIV p24 peptides are described in WO91/13360, wherein the peptides are used in a method of discriminating between a false and true diagnosed HIV-positive serum sample.

Johnson R.P., et al., The Journal of Immunology, Vol.147, p.1512-1521, No.5, September 1, 1991 describe an analysis of the fine specificity of gag-specific CTL-responses in three HIV-1 seropositive individuals, the gag-specific CTL-responses were found to be mediated by CD3+ CD8+ lymphocytes which are HLA class I restricted. Goulder P.J.R. et.al., Journal of Virology, Vol. 74, p.5679-5690, No 12, June 2000 has studied CTL response from different parts of p17 and p24 of HIV in different populations. The findings show that certain immunodominant regions exist, however, minor differences in amino acid composition can cause large differences in response.

EP-A-0 356 007 discloses antigenic determinants, in particular it relates to synthetic polypeptide sequences which are related to proteins present in the HIV-1 and which can be used as a basis for a potential vaccine against AIDS.

Rosenberg E.S. et al., Science, Vol.278, 21 November 1997, p.1447-1450 describe that virus specific CD4+ T helper lymphocytes are critical to the maintenance of effective immunity in a number of chronic viral infections, but are characteristically undetectable in chronic human immunodeficiency virus-type 1 (HIV-1) infection. HIV-1-specific proliferative responses to p24 were inversely related to viral load. They conclude that the HIV-1-specific helper cells are likely to be important in immunotherapeutic interventions and vaccine development.

EP 0 230 222, EP 0 270 114, DE 37 11 016 and GB 2 188 639 all in the name of F. Hoffmann-La Roche & Co. Aktiengesellschaft concern recombinant expression and purification of an HTLVIII Gag/Env gene protein or fusion proteins. The proteins consisting of native sequences can be purified to homogeneity and used as a basis for diagnostic tests for detection of antibodies against viruses associated with AIDS. The gag/env protein may also be formulated for use as a vaccine for protection against AIDS through prophylactic immunization.

From a diagnostic and therapeutic point of view, the major problems with using p24 as part of an assay or therapy is associated with the high number of epitopes on p24 which stimulates production of a large number of antibodies with poor specificity, which through repeated boostering on potential mutated sequences can create autoantibodies (Autoantibodies to the alfa/beta T-cell receptors in HIV infection; dysregulation and mimicry. Lake D.F., et al., Proc. Natl. Acad. Sci. USA, (23) : 10849-53, Nov. 8 1994). Further, it is reported that the p24 antibody titer does not reach the same high levels as for the envelope proteins (gp120 and gp41). Normally antibodies to p24 are developed in the very early phase of the infection, but the titer is fairly quickly stabilized after the initial infection period. Later the p24 titer is gradually decreasing while the opposite happens with gp160. These findings can also be seen in relation to recent reports stating that cytotoxic T-cell activity is antagonized by naturally occurring HIV-1 gag variants (Klenerman P., et al., Nature, 2:369 (6479), p. 355, 2 June 1994). This can be one of the reasons why a rapid stabilization of the p24 titer is seen and why it later starts to decrease.

Based on the above background data, we decided to investigate the possibility of designing novel synthetic peptides which can mimic the p17 and p24 epitopes without antagonizing the cytotoxic T-cell activity, in order to meet the need for an effective prophylactic and therapeutic vaccine.

The sequence of p17 identified as a possible template for development of peptides that can elicit CTL and antibody response is published by Korber B., et al., Human Retroviruses and AIDS 1999 Eds.Theoretical Biology and Biophysics Group, Los Alamos National Laboratory, Los Alamos, NM. The identified amino acid sequence is located between the amino acids 33 and 53, confer table 1:

Table 1

AA no.	AA sequence	Naturally occurring AA's				
33	H					
34	I	L	V	M		
35	I	V				
36	W					
37	A					
38	S	N	R			
39	R	S				
40	E					
41	L	M				
42	E	D	K	G	Q	
43	R	K	G	N		
44	F	S	Y			
45	A	T	S			
46	V	L	I	C		
47	N	D	S			
48	P	R	S	T		
49	G	S	A	D	N	Q
50	L	F				
51	L	M				
52	E	G	D			
53	T	S	A			

The one letter as well as the three letter codes defining the amino acids in the sequences given throughout this specification are in accordance with International standards and given in textbooks, for instance Lehninger A.L., «Principles of Biochemistry», Worth Publishers Inc., New York, 1982. The amino acids given to the right of the second column represent the natural variation of the sequence. A change in the overall charge of the epitope by modification of amino acids can involve a significant improvement of the immunogenicity. The modifications involve a probable conformation change from the original helical to a sheet structure, exposing the epitope to the immune system in a different manner and expectingly to a greater extent.

To further increase the number of T-cell epitopes and reduce the probability for development of escape mutants within the gag protein three additional peptide

sequences from p24 were based on the following three sequences from residues 133-158, 178-199 and 233-251, respectively published in Human Retroviruses and AIDS 1999; A Compilation and Analysis of Nucleic Acid and Amino Acid Sequences. Eds.Theoretical Biology and Biophysics Group, Los Alamos National Laboratory, Los Alamos, confer tables 2-4 :

Table 2

AA no.	AA sequence	Naturally occurring AA's at each AA position			
133	P				
134	I	V	L		
135	V	M	A	I	
136	Q	S	T	V	
137	N	D	T		
138	I	A	L	M	
139	Q	E	K	G	
140	G				
141	Q	I			
142	M	P	A		
143	V	I	A	T	R
144	H				
145	Q	H			
146	A	S	V	N	P
147	I	L	M	V	
148	S	T			
149	P	A			
150	R				
151	T				
152	L	S			
153	N	F			
154	A				
155	W				
156	V				
157	K				
158	V	A	C		

Table 3

AA no.	AA sequence	Naturally occurring AA's at each AA position				
178	G					
179	A					
180	T	A	I	V	L	
181	P	S				
182	Q	H	G	T	S	Y
183	D					
184	L	I	V			
185	N	Y				
186	T	M	L	A		
187	M					
188	L					
189	N	S	T			
190	T	I	V	A		
191	V	I				
192	G					
193	G	D				
194	H					
195	Q					
196	A	G				
197	A					
198	M	L				
199	Q	E	H			

and

Table 4

AA no.	AA sequence	Naturally occurring AA's at each AA position
233	G	
234	S	A
235	D	
236	I	
237	A	
238	G	

Table 4 cont.

239	T	A	S					
240	T	S						
241	S	T						
242	T	N	S					
243	L	P	V	Q				
244	Q	A	H					
245	E							
246	Q	H						
247	I	L	V	M				
248	G	A	Q	T	N	R	H	I
249	W							
250	M	T						
251	T	S						

Several modified peptides have been synthesized in order to determine unique sequences which are both specific and sensitive towards HIV-1.

DESCRIPTION OF THE INVENTION

The peptides according to the invention are originating from the four different conserved areas of the HIV-1 gag protein p17 and p24 which are described above, having the properties of maintaining the uniqueness of the HIV-1-epitope. Further the new peptides according to the invention possess no recognized cytotoxic T lymphocyte (CTL) antagonistic effect and shall have at least one potential CTL epitope.

The peptides, according to the invention, which have met the above criteria are selected from the following groups ;

$Xaa_1\ Xaa_2\ Xaa_3\ Xaa_4\ Xaa_5\ Xaa_6\ Xaa_7$Gln Leu Gln $Xaa_{11}\ Xaa_{12}\ Xaa_{13}\ Xaa_{14}\ Xaa_{15}\ Xaa_{16}$ $Xaa_{17}\ Xaa_{18}\ Xaa_{19}\ Xaa_{20}\ Xaa_{21}$ (SEQ ID NO : 1)

wherein the amino acids of the chain could have the following meanings ;

Xaa in position 1 of the peptide derivate is His, Lys or Arg,

Xaa in position 2 is Ile, Leu, Val or Met,

Xaa in position 3 is Ile or Val,
Xaa in position 4 is Trp or Tyr,
Xaa in position 5 is Ala or Leu,
Xaa in position 6 is Ser, Thr, Arg or Asn,
Xaa in position 7 is Arg or Ser,
Xaa in position 11 is Arg, Lys, Gly or Asn,
Xaa in position 12 is Phe, Ser or Tyr
Xaa in position 13 is Ala, Thr or Ser
Xaa in position 14 is Val, Leu, Ile or Cys,
Xaa in position 15 is Asn, Asp or Ser,
Xaa in position 16 is Pro, Arg or Ser,
Xaa in position 17 is Gly, Ser, Ala, Asp or Asn
Xaa in position 18 is Leu or Phe,
Xaa in position 19 is Leu or Met,
Xaa in position 20 is Glu, Gly, Asp or Ile,
Xaa in position 21 is Thr, Ser or Ala
the peptide comprises at least six consecutive amino acids of the sequence of SEQ ID NO : 1,

$Xaa_1\ Xaa_2\ Xaa_3\ Xaa_4\ Xaa_5\ Xaa_6\ Xaa_7$ Gly Xaa_9 Leu Val –Z- Tyr $Xaa_{13}\ Xaa_{14}\ Xaa_{15}\ Xaa_{16}\ Xaa_{17}\ Xaa_{18}\ Xaa_{19}\ Xaa_{20}\ Xaa_{21}$ Ala $Xaa_{23}\ Xaa_{24}\ Xaa_{25}\ Xaa_{26}$ (SEQ ID NO : 4)

wherein the amino acids of the chain have the following meaning;
Xaa in position 1 is Pro, Tyr or Phe
Xaa in position 2 is Ile, Val or Leu,
Xaa in position 3 is Ile, Ala, Val, Met or Leu
Xaa in position 4 is Gln, Ser, Thr or Val
Xaa in position 5 is Asn, Asp or Thr
Xaa in position 6 is Ile, Ala, Leu or Met
Xaa in position 7 is Gln, Glu Lys or Gly
Xaa in position 9 is Gln or Ile
Xaa in position 13 is omitted
Xaa in position 14 is Ala, Ser, Asn, Val or Pro
Xaa in position 15 is Ile, Leu, Met or Val,
Xaa in position 16 is Ser or Thr

Xaa in position 17 is Pro or Ala,
Xaa in position 18 is Arg or Lys,
Xaa in position 19 is Thr or Ser
Xaa in position 20 is Leu or Ser
Xaa in position 21 is Asn, Phe or Val,
Xaa in position 23 is Trp, Tyr, Gly or none
Xaa in position 24 is Val, Leu, Gly or none
Xaa in position 25 is Lys, Arg, Gly or none
Xaa in position 26 is Val, Ala, Cys, Gly or none
wherein the sequence of SEQ ID NO : 4 comprises at least six consecutive amino acids and –Z- is optional and have the meaning PEG, modified PEG and/or $[Gly]_n$, wherein n = 1, 2 or 3,

Xaa_1 Ala Xaa_3 Xaa_4 Xaa_5 Ala Xaa_7 Xaa_8 Xaa_9 Leu Leu Xaa_{12} Xaa_{13} Xaa_{14} –Z- Xaa_{15} Xaa_{16} His Gln Xaa_{19} Ala Xaa_{21} Xaa_{22} (SEQ ID NO : 9)

wherein Xaa in position 1 is Tyr, Trp, Phe or Gly
Xaa in position 3 is Thr, Ala, Val, Ile or Leu
Xaa in position 4 is Pro or Ser
Xaa in position 5 is Gln, His, Gly, Thr, Ser or Tyr
Xaa in position 7 is Leu, Ile or Val
Xaa in position 8 is Asn or Tyr
Xaa in position 9 is Thr, Met, Leu or Ala
Xaa in position 12 is Ser, Thr or Asn
Xaa in position 13 is Thr, Ile, Val or Ala
Xaa in position 14 is Val or Ile
Xaa in position 15 is Gly or none
Xaa in position 16 is Gly or none
Xaa in position 19 is Ala or Gly
Xaa in position 21 is Met, Leu, Cys or none
Xaa in position 22 is Gln, Glu, His, Gly or none
wherein the sequence of SEQ ID NO : 9 consists of at least six consecutive amino acids and the linker –Z- is optional and have the meaning PEG, modified PEG and/or $[Gly]_n$, wherein n = 1, 2 or 3,

$Xaa_1\ Xaa_2$ Ala Leu Ala Gly $Xaa_7\ Xaa_8\ Xaa_9$ Leu $Xaa_{11}\ Xaa_{12}\ Xaa_{13}\ Xaa_{14}\ Xaa_{15}\ Xaa_{16}$ $Xaa_{17}\ Xaa_{18}\ Xaa_{19}\ Xaa_{20}\ Xaa_{21}$ (SEQ ID NO : 15)

wherein the Xaa in position 1 is Trp or Tyr
Xaa in position 2 is Ser or Ala
Xaa in position 7 is Thr, Ala or Ser
Xaa in position 8 is Ser or Thr
Xaa in position 9 is Ser or Thr
Xaa in position 11 is Leu, Pro, Val or Gln
Xaa in position 12 is Gln, Ala or His
Xaa in position 13 is Glu or Gly
Xaa in position 14 is Gln or His
Xaa in position 15 is Ile, Leu, Val or Met
Xaa in position 16 is Gly, Ala, Gln, Thr, Asn, Arg, His or Ile
Xaa in position 17 is Trp or Tyr
Xaa in position 18 is Thr, Met, Leu or Ile
Xaa in position 19 is Thr or Ser
Xaa in position 20 is Cys, Gly or none
Xaa in position 21 is Gly or none
wherein the sequence of SEQ ID NO : 15 consists of at least six consecutive amino acids,
the terminal ends of the sequences may be free carboxyl- or amino groups, amides, acyls, acetyls or salts thereof,
two or more of the Cys residues may form part of an interchain disulphide binding, a -S-$(CH_2)_p$-S- or a - $(CH_2)_p$-bridge wherein p = 1-8, optionally intervened by one or more hetero atoms such as O, N or S and/or the said peptide sequences are immobilized to a solid support.

The new peptide sequences have the potential to serve as a good antigen wherein the antigen comprises at least one peptide selected from the group of sequences of SEQ ID NO : 1, SEQ ID NO : 4, SEQ ID NO : 9 or SEQ ID NO : 15 . The antigenicity may be adapted through adjusting the ratio or concentration of different peptides or size of the peptides by for instance dimerization or polymerization and/or immobilization to a solid phase. The antigen comprises two or more polypeptide sequences, according to the invention, which are either linked by a bridge for instance a disulphide bridge between

the Cys residues of the chains or bridges like C_1-C_8 alkylen possibly intervened by one or more heteroatoms like O, S, or N or preferably they are unlinked. The chains may be immobilized to a solid phase in monomeric, dimeric or oligomeric forms. Further amino acids may be added to the ends in order to achieve an «arm» to facilitate immobilization.

PEG is polyethylene glycol ($HO(CH_2CH_2O)_mH$ and can be part of the linker –Z-, optionally PEG is modified by a dicarboxylic acid ($HO(CH_2CH_2O)_mCO(CH_2)_oCOOH$) or a terminal carboxylic group ($HO(CH_2CH_2O)_{m-1}CH_2COOH$) where m= 1-10 and o=2-6, prior to linking.

The linker –Z- can either consist of PEG, modified PEG, or a combination thereof and/or one or more Gly residues combined. Alternatively the linker –Z- can consist of a Gly-bridge $[Gly]_n$ where n=1, 2 or 3.

All amino acids in the peptides of the invention can be in both D- or L-form, although the naturally occurring L- form is preferred.

The C- and N-terminal ends of the peptide sequences could deviate from the natural sequences by modification of the terminal NH_2-group and/or COOH-group, they may for instance be acylated, acetylated, amidated or modified to provide a binding site for a carrier or another molecule.

The peptides according to the invention are consisting of at least 6 amino acids, preferably between 10 and 30 amino acids. They are covering all natural variation of amino acids in the identified positions.

The polypeptide antigen according to the invention is either in a free or in a carrier-bound form. The carrier or solid phase to which the peptide is optionally bound can be selected from a vide variety of known carriers. It should be selected with regard to the intended use of the immobilized polypeptide as a diagnostic antigen or as an immunizing component in a vaccine.

Examples of carriers that can be used for e.g. diagnostic purposes are magnetic beads or latex of co-polymers such as styrene-divinyl benzene, hydroxylated styrene-divinyl

benzene, polystyrene, carboxylated polystyrene, beads of carbon black, non-activated or polystyrene or polyvinyl chloride activated glass, epoxy-activated porous magnetic glass , gelatine or polysaccharide particles or other protein particles, red blood cells, mono or polyclonal antibodies or fab fragments of such antibodies.

According to a further embodiment of the present invention, the antigens may form part of a vaccine possibly combined with carriers, adjuvants or combined with other immunostimulating elements such as canarypox virus carrying the *env* gene. Examples of carriers and/or adjuvants for vaccine purposes are other proteins such as human or bovine serum albumin and keyhole limpet haemocyanin and fatty acids. Immunostimulatory materials may be divided into three groups; adjuvants, carriers for antigens and vehicles. Examples of adjuvants include aluminum hydroxyd, aluminum salts, saponin, muramyl di and tripeptides, monophosphoryl lipid A, palmitic acid, *B.pertussis* and various cytokines including the Th1 cytokine IL-12 and IL-1. A number of protein toxins can be used to carry passenger proteins across cellular membranes into the cytosol, which are useful in developing CTL vaccines. Carriers include bacterial toxoids such as inactivated tetanus and cholera toxins, genetically detoxified bacterial toxins such as heat labile enterotoxin from *E.coli*, fatty acids, live vectors such as polio chimeras and hybrid proteins that form particulates for example yeast retrotransposon hybrid TY particles and HBcAg particles. Vehicles which are frequently occurring components in modern vaccines are consisting of mineral oil emulsion, Freunds complete and incomplete adjuvant, vegetable oil emulsions, nonionic block co-polymer surfactants, squalene or squalane, lipopeptides, liposomes and biodegradable microspheres. Two recent adjuvants which possess significant potential for the development of new vaccines include an oil-in- water microemulsion (MF59) and polymeric microparticles. Any substance that can enhance the immunogenicity of the antigen may be used and several further alternatives of carriers or adjuvants are given in the US or European Pharmacopoeia.

A suitable formulation of the antigen for immunostimulatory uses may also comprise interferons such as INF-γ, antiviral chemokines or haematopoietic growth factors such as granulocyte macrophage growth (colony stimulating) factor.

Another approach in order to enhance the stimulation and absorption in for instance the intestine is to administer the peptides of the invention, with small peptides such as di, tri

or tetrapeptides. These peptides can be administered in addition to or in combination with the peptides of the invention. Preferably the peptides are administered together with the tripeptide YGG, consisting of amino acids in the D- or L-forms, preferably in the D-form.

Recent approaches to non-parenteral delivery of vaccines, for instance via mucosa include; gene fusion technology to create non-toxic derivatives of mucosal adjuvants, genetically inactivated antigens with a deletion in an essential gene, co-expression of an antigen and a specific cytokine that is important in the modulation and control of a mucosal immune response, and genetic material itself that would allow DNA or RNA uptake and its endogenous expression in the host cells.

One approach for developing durable responses where cell-mediated immunity is required, is to vaccinate with plasmid DNA encoding one or more specific antigen(s).

In order to protect against HIV infection, vaccines should induce both mucosal and systemic immune responses and could be administered by any convenient route, parenterally or non-parenterally, such as subcutanously, intracutanously, intravenously, intramuscularly, perorally, mucosally or intranasally for example.

In a preferred embodiment of the vaccine according to the present invention it comprises antigens containing at least one of the peptides selected from the groups of SEQ ID NO : 1, 4, 9 and 15, more preferred different peptides occur in equal amounts.

In a further preferred embodiment the vaccine composition contains the antigens ;

R L I Y A T R Q L Q R F A V N P G L L I T - NH_2 (SEQ ID NO : 3)

F I L Q N I E G Q L V G G G Y A I S P R T L V A G G G G (SEQ ID NO : 6)

Y A I P Q A L N T L L N T V G G H Q A A - NH_2 (SEQ ID NO : 11)

and

W S A L A G T T S L L Q G Q L G W I T - NH_2 (SEQ ID NO : 14)

The sequences contribute with CTL-epitopes and can activate the cellular immune system. The amino acid changes implemented within the frame of the CTL-epitopes are designed to achieve enhanced binding. Other amino acid changes have been conducted in order to facilitate the synthesis of the peptide and/or to increase the solubility of the peptide.

A method for detecting antibodies, induced by HIV-1 or HIV-1 specific peptides or proteins, in a sample of body fluid using the present antigens is a further embodiment of the invention. Also immunoassay kit designed for this detection and antibodies capable of selectively reacting with the said antigens are encompassed by the present invention.

DESCRIPTION OF THE PREPARATION OF THE PEPTIDES

The peptides of the invention can be produced by any known method of producing a linear amino acid sequence, such as recombinant DNA techniques. A nucleic acid sequence which encodes a peptide of the invention or a multimer of the said peptides, is introduced into an expression vector. Suitable expression vectors are for instance plasmids, cosmids, viruses and YAC (yeast artificial chromosome) which comprise necessary control regions for replication and expression. The expression vector may be stimulated to expression in a host cell. Suitable host cells are for example bacteria, yeast cells and mammalian cells. Such techniques are well known in the art and described for instance by Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, 1989. Other well-known techniques are degradation or synthesis by coupling of one amino acid residue to the next one in liquid phase or preferably on a solid phase (resin) for instance by the so-called Merrifield synthesis. See for instance Barany and Merrifield in the Peptides, Analysis, Synthesis, Biology, Vol.2, E. Gross and Meinhofer, Ed. (Acad.Press, N.Y., 1980), Kneib-Coronier and Mullen Int. J. Peptide Protein Res.,30, p.705-739 (1987) and Fields and Noble Int.J.Peptide Protein Res., 35, p.161-214 (1990).

In case a linked or cyclic peptide is desired, the amino acid sequence is subjected to a chemical oxidation step in order to cyclize or link the two cysteine residues between two peptide sequences, when the appropriate linear amino acid sequences are synthesized, see Akaji et al., Tetrahedron Letter, 33, 8, p.1073-1076, 1992.

GENERAL DESCRIPTION OF SYNTHESIS

All peptide derivatives prepared in the Examples given below were synthesized on a Milligen 9050 Peptide Synthesizer using a standard program. The resin used was Tenta Gel P RAM with a theoretical loading of 0,20 meq/g (RAPP POLYMERE GmbH, Tübingen). The final product of the synthesis was dried *in vacuo* overnight. The peptide was then cleaved from the resin by treatment with 90% trifluoroacetic acid in the presence of ethane dithiol (5%) and water (5%) as scavengers (1,5 hours at RT). Then the resin was filtered and washed on filter with additional trifluoroacetic acid (100%) (2 x 20 ml). The combined filtrates were evaporated *in vacuo* (water bath at RT) and the residue was triturated with ethyl ether (200 ml) and the precipitated product filtered off. The solid was promptly dissolved on filter with glacial acetic acid (100 ml) and added to 1,5 l of 20% acetic acid in methanol and treated with 0,1 M solution of iodine in methanol until a faint brown colour remained. Then Dowex 1 x 8 ion exchange in acetate form (15g) (Bio-Rad, Richmond, CA) was added and the mixture filtered. The filtrate was evaporated and the residue freeze-dried from acetic acid. The product was then purified by reversed phase liquid chromatography on a column filled with Kromasil® 100 - 5 C8 (EKA Nobel, Surte, Sweden) in a suitable system containing acetonitrile in 0,1 % trifluoroacetic acid water solution. The samples collected from the column were analyzed by analytical high performance liquid chromatography (HPLC) (Beckman System Gold, USA) equipped with a Kromasil® 100 - 5 C8 Column (EKA Nobel, Surte, Sweden). Fractions containing pure substance were pooled, the solvent was evaporated and the product freeze-dried from acetic acid. The final HPLC analysis was performed on final product, and the structure of the peptide was confirmed by amino acid analysis and mass spectrometry (LDI-MS).

All amino acids used during the synthesis were L-amino acids and they were protected with a fluorenylmethoxy-carbonyl group at the α-amino function. The side chains were protected as follows :

Cys (Trt), Gln(Trt), Glu(OtBu), Thr(tBu).

The abbreviations, within the brackets are :
Trt = triphenylmethyl
t-Bu = tert. Butyl
OtBu = tert. Butylester

The amino acid derivatives was supplied by Bachem AG, Switzerland.

EXAMPLE 1

Preparation of H L I Y L T R Q L Q R F A L N P G L L I T - NH_2 (SEQ ID NO : 2).
The peptide is synthesized in amide form, from corresponding starting materials according to the general description of synthesis. The purity is determined by HPLC analysis and the structure is confirmed by amino acid analysis and mass spectrometry (LDI-MS).

EXAMPLE 2

Preparation of R L I Y A T R Q L Q R F A V N P G L L I T-NH_2 (SEQ ID NO : 3).
The peptide was synthesized in amide form, from corresponding starting materials according to the general description of synthesis. The purity was determined by HPLC analysis and the structure was confirmed by amino acid analysis and mass spectrometry (LDI-MS).
Purity (HPLC) : more than 97% (single impurities less than 1%)
Molecular weight (free base) : 2442.9

EXAMPLE 3

Preparation of Y I L Q N I E G Q L V G G G Y A I S P R T L V A Y L R G - NH_2 (SEQ ID NO : 5). The peptide is synthesized in amide form, from the corresponding starting materials according to the general description of synthesis. The purity is determined by HPLC analysis and the structure is confirmed by amino acid analysis and mass spectrometry (LDI-MS).

EXAMPLE 4

Preparation of F I L Q N I E G Q L V G G G Y A I S P R T L V A G G G G (SEQ ID NO : 6). The peptide was synthesized from the corresponding starting materials according to the general description of synthesis. The purity was determined by HPLC analysis and the structure was confirmed by amino acid analysis and mass spectrometry (LDI-MS).
Purity (HPLC) : more than 94 %
Molecular weight (free base) : 2745
Molecular formula : $C_{123}H_{198}O_{37}N_{34}$

EXAMPLE 5 - REFERENCE EXAMPLE

Preparation of a nativ p24 sequence P I V Q N I E G Q M V H Q A I S P R T L N A W V K V (SEQ ID NO : 7). The peptide was synthesized from the corresponding starting materials according to the general description of synthesis. The purity was determined by HPLC analysis and the structure was confirmed by amino acid analysis and mass spectrometry (LDI-MS).

Purity (HPLC) : approx. 85 %

Molecular weight (free base) : 2929

Molecular formula : $C_{131}H_{214}O_{36}N_{38}$ S

EXAMPLE 6

Preparation of F I L Q N I Q G Q L V G G G Y A I S P R T L V A G - NH_2 (SEQ ID NO : 8).

The peptide was synthesized in amide form, from corresponding starting materials according to the general description of synthesis. The purity was determined by HPLC analysis and the structure was confirmed by amino acid analysis and mass spectrometry (LDI-MS).

Purity (HPLC): more than 97 % (single impurity less than 1%)

Molecular weight (free base): 2572.0

EXAMPLE 7 – REFERENCE EXAMPLE

Preparation of a nativ p24 sequence G A T P Q D L N T M L N T V G G H Q A A - NH_2 (SEQ ID NO : 10). The peptide was synthesized in amide form, from the corresponding starting materials according to the general description of synthesis. The purity was determined by HPLC analysis and the structure was confirmed by amino acid analysis and mass spectrometry (LDI-MS).

Purity (HPLC) : 98 %

Molecular weight (free base) : 1995.2

Molecular formula : $C_{82}H_{135}O_{29}N_{27}$ S

EXAMPLE 8

Preparation of Y A I P Q A L N T L L N T V G G H Q A A - NH_2 (SEQ ID NO : 11).

The peptide was synthesized in amide form, from the corresponding starting materials according to the general description of synthesis. The purity was determined by HPLC

analysis and the structure was confirmed by amino acid analysis and mass spectrometry (LDI-MS).

Purity (HPLC) : 98 %

Molecular weight (free base) : 2051.4

Molecular formula : $C_{91}H_{147}O_{27}N_{27}$

EXAMPLE 9

Preparation of F A I P Q A L N T L L N T V G G G G H Q A A C G - NH_2 (SEQ ID NO : 12). The peptide is synthesized in amide form, from the corresponding starting materials according to the general description of synthesis. The purity is determined by HPLC analysis and the structures is confirmed by amino acid analysis and mass spectrometry (LDI-MS).

EXAMPLE 10 – REFERENCE EXAMPLE

Preparation of a nativ p24 sequence G S D I A G T T S T L Q E Q I G W M T - NH_2 (SEQ ID NO : 13). The peptide was synthesized in amide form, from the corresponding starting materials according to the general description of synthesis. The purity was determined by HPLC analysis and the structure was confirmed by amino acid analysis and mass spectrometry (LDI-MS).

Purity (HPLC) : 90 %

Molecular weight (free base) : 1995.2

Molecular formula : $C_{84}H_{135}O_{31}N_{23}$ S

EXAMPLE 11

Preparation of W S A L A G T T S L L Q G Q L G W I T - NH_2 (SEQ ID NO : 14). The peptide was synthesized in amide form, from the corresponding starting materials according to the general description of synthesis. The purity was determined by HPLC analysis and the structure was confirmed by amino acid analysis and mass spectrometry (LDI-MS).

Purity (HPLC) : more than 97% (single impurities less than 1%)

Molecular weight (free base) : 2007.3

EXAMPLE 12 - REFERENCE EXAMPLE

Preparation of a nativ p17 sequence H I V W A S R E L E R F A V N P G L L E V T – NH_2 (SEQ ID NO : 16). The peptide was synthesized in amide form, from corresponding starting materials according to the general description of synthesis. The purity was determined by HPLC analysis and the structure was confirmed by amino acid analysis and mass spectrometry (LDI-MS).

Purity (HPLC) : more than 95%

Molecular weight (free base) : 2436.8

EXAMPLE 13 - REFERENCE EXAMPLE

Preparation of a nativ p24 sequence P I V Q N I Q G Q M V H Q A I S P R T L N A W – NH_2 (SEQ ID NO : 17). The peptide was synthesized in amide form, from corresponding starting materials according to the general description of synthesis. The purity was determined by HPLC analysis and the structure was confirmed by amino acid analysis and mass spectrometry (LDI-MS).

Purity (HPLC) : approximately 93%

Molecular weight (free base) : 2601.0

EXAMPLE 14

Dimerisation via disulphide bridge.

The peptide sequences are linked via an oxidation step to form a dipeptide wherein the cysteine residues form a disulphide bridge. The bridge can for instance be formed by oxidation with I_2 as follows ;

Equal amounts of the peptides are dissolved in acetic acid/methanol (1:4) and 0,1 M I_2 in methanol is added yielding a mixture of the dimer.

EXAMPLE 15

A vaccine comprising the peptides of the SEQ ID NO : 3, 6, 11 and 14 is prepared. The freeze-dried peptides are dissolved in sterile water at a final concentration of 4 mg/ml. The final salt concentration of the solution is physiological compatible. A preparation of a granulocyte-macrophage-colony stimulating factor (GM-CSF) is also prepared, according to the manufacturers directions for use, to a final concentration of 0,3 mg/ml. The two solutions are administered intracutaneously. A typical injection dose is 100 µl.

EXAMPLE 16

An antigen solution or suspension is mixed with equal parts of Freund's adjuvant of Behring, complete or incomplete, and is then finely emulsified by being drawn up into, and vigorously pressed out of, an injection syringe, or with a homogenator. The emulsion should remain stable for at least 30 minutes. The antigen-adjuvant emulsions is best injected subcutaneously as a depot.

EXAMPLE 17

Immunoassay for detection of antibodies induced by HIV-1.

The magnetic particle reagents are to be prepared according to the manufacturers recommended protocol. Dynal AS, is the manufacturer of the Dynabeads, which are employed. The magnetic particles coated with ligand are called Reagent 1. A peptide according to the invention is covalently coupled to the pre-activated surface of the magnetic particles. It is also possible to physically absorb the peptide to the surface of the magnetic particles. The concentration of particles in Reagent 1 is within the range from 1 mg/ml to 15 mg/ml. The particle size varies between 0,2 μm to 15 μm. The concentration of peptides is within the range from 0,01 mg/mg particle to 1 mg/mg particle.

The anti human Ig Alkaline Phosphatase (AP) conjugated antibody reagent is prepared according to the recommended protocol of Dako AS. This protocol is a standard procedure in this field. This reagent is called Reagent 2.

The substrate solution phenolphtalein-monophosphate is to be prepared according to the recommended protocol of Fluka AG. This protocol is a standard procedure in this field. The substrate solution is called Reagent 3.

The washing and incubation buffer which is used is standard 0,05 M tris-base buffer with the following additional compounds; Tween 20 (0,01% to 0,1%), glycerol (0,1% to 10%) and sodium chloride (0,2% to 0,1%).

The assay procedure comprises an incubation step wherein 1 drop of Reagent 1 is mixed with 2 drops of washing buffer in each well. After mixing, 30 μl of sample is added and the solution is incubated for 5 minutes. The magnetic particles can be trapped by a magnet and the liquid removed, before the magnet is separated. Then the wells are washed twice in 4 drops of washing solution, before incubation with Reagent 2. 1 drop of Reagent 2 is added with 2 drops of washing buffer and the solution is incubated for 5 minutes. The magnetic particles can be trapped by a magnet and the

liquid removed, before the magnet is separated. Then the washing step is repeated before incubation with Reagent 3. 2 drops of Reagent 3 is added to each well and the solution is incubated for 3 minutes. The results can be read against a white background. Positive results are red (3+ = strong red) whereas negative results are clearly light yellow/brown solutions as obtained in the negative control.

The immunoassay kit could be used in detection of antibodies, induced either by HIV virus or HIV-specific peptides or proteins, for instance the peptides of the present invention.

EXAMPLE 18

Therapeutic or prophylactic vaccine

At least one of the polypeptides of the invention, selected from the group of sequences, SEQ ID NO : 1, SEQ ID NO : 4, SEQ ID NO : 9 and SEQ ID NO : 15 can be used to form antigens and be the active principle of a prophylactic or therapeutic vaccine intended to provide protection against the human immunodeficiency virus type 1 (HIV-1). The vaccine may include compounds having beneficial effects in protecting or stimulating the hosts immune system (human being or vertebrate animal) for instance interleukins, interferons, granulocyte macrophage growth factors, haematopoietic growth factors or similar. Preferably the vaccine composition further contain an adjuvant or vehicle, more preferably the adjuvant or vehicle is Monophosphoryl Lipid A (MPL ®) possibly with alum, Freund`s adjuvant (complete or incomplete) or aluminum hydroxyd. The optimal amount of adjuvant/vehicle will depend on the type(s) which is/are chosen.

The peptides of the invention might be modified by C-terminal addition of a single fatty acid such as a single palmitoyl chain to form a lipopeptide vaccine. Further the lipopeptides can be introduced into liposome membranes by the freeze-thaw method resulting in liposomes bearing the peptide ligands on their surface.

The peptide or vaccine formulation can be freeze-dried prior to storage. The freeze-dried peptides can be dissolved in sterile water to a final concentration of from 0,1 to 100 mg/ml. The vaccine may be stored preferably at low temperature, in ampoules containing one or more dosage units, ready for use. A typical dosage unit of the peptide according to the invention is within the concentration range : 0,05 μg-1mg per kg bodyweight, preferably within 0,15 μg-ก 15 mg per kg body weight. Persons skilled in

the art will appreciate that a suitable dose will depend on the body weight of the pasient, the type of disease, severity of condition, administration route and several other factors. When used as a therapeutic vaccine the vaccine will typically initially be administered about 12 times, through injections. Further boosters might follow and in extreme cases be administered throughout the patients life. In preparation of an injection solution the peptides are dissolved in sterile water to a final concentration of 1 mg/ml per peptide. Typically an injection volume is 100 µl to 200 µl (2 x 100 µl). The peptide is preferably co-administered with a suitable adjuvant and/or a granulocyte-macrophage growth factor, for instance Leucomax® «Shering Plough» made within a concentration range of from 0,1 to 1 mg/ml, or according to the manufacturers recommendations. Particulary preferred is a combination therapy where the present peptides are administered together with the peptides described in the published International patent application no. PCT/NO00/00075 filed March 2, 2000 and/or the co pending Norwegian Patent Application No. 2000 4412. The peptides may be administered sequentially or simultaneously. Suitable administration may be intracutane, subcutane, intravenous, peroral, intramuscular, intranasal, mucosal or any other suitable route. Booster administrations may be required in order to maintain protection. For persons skilled in the art it will be understood that the vaccine compositions according to the invention are useful not only in prevention of infection, but also in treatment of infection.

No toxic effects of the peptides according to the invention, are observed when injected in mice in a dosage of 100 µg per kg body weight.

The above Examples are only meant as illustrating the invention. It must be understood that a person skilled in the art can modify the peptides, antigens and vaccines herein described without deviating from the concept and scope of this invention as set forth in the claims.

PATENT CLAIMS

1. Peptide characterized in that it comprises at least one amino acid sequence selected from the groups of amino acid sequences :

$Xaa_1\ Xaa_2\ Xaa_3\ Xaa_4\ Xaa_5\ Xaa_6\ Xaa_7$Gln Leu Gln $Xaa_{11}\ Xaa_{12}\ Xaa_{13}\ Xaa_{14}\ Xaa_{15}\ Xaa_{16}\ Xaa_{17}\ Xaa_{18}\ Xaa_{19}\ Xaa_{20}\ Xaa_{21}$ (SEQ ID NO : 1)

wherein the amino acids of the chain could have the following meanings ;
Xaa in position 1 of the peptide derivate is His, Lys or Arg,
Xaa in position 2 is Ile, Leu, Val or Met,
Xaa in position 3 is Ile or Val,
Xaa in position 4 is Trp or Tyr,
Xaa in position 5 is Ala or Leu,
Xaa in position 6 is Ser, Thr, Arg or Asn,
Xaa in position 7 is Arg, or Ser,
Xaa in position 11 is Arg, Lys, Gly or Asn,
Xaa in position 12 is Phe, Ser or Tyr
Xaa in position 13 is Ala, Thr or Ser
Xaa in position 14 is Val, Leu, Ile or Cys,
Xaa in position 15 is Asn, Asp or Ser,
Xaa in position 16 is Pro, Arg or Ser,
Xaa in position 17 is Gly, Ser, Ala, Asp or Asn
Xaa in position 18 is Leu or Phe,
Xaa in position 19 is Leu or Met,
Xaa in position 20 is Glu, Gly, Asp or Ile,
Xaa in position 21 is Thr, Ser or Ala

the peptide comprises at least six consecutive amino acids of the sequence of SEQ ID NO : 1,

$Xaa_1\ Xaa_2\ Xaa_3\ Xaa_4\ Xaa_5\ Xaa_6\ Xaa_7$ Gly Xaa_9 Leu Val –Z- Tyr $Xaa_{13}\ Xaa_{14}\ Xaa_{15}\ Xaa_{16}\ Xaa_{17}\ Xaa_{18}\ Xaa_{19}\ Xaa_{20}\ Xaa_{21}$ Ala $Xaa_{23}\ Xaa_{24}\ Xaa_{25}\ Xaa_{26}$ (SEQ ID NO : 4)

wherein the amino acids of the chain have the following meaning;

Xaa in position 1 is Pro, Tyr or Phe
Xaa in position 2 is Ile, Val or Leu,
Xaa in position 3 is Ile, Ala, Val, Met or Leu
Xaa in position 4 is Gln, Ser, Thr or Val
Xaa in position 5 is Asn, Asp or Thr
Xaa in position 6 is Ile, Ala, Leu or Met
Xaa in position 7 is Gln, Glu Lys or Gly
Xaa in position 9 is Gln or Ile
Xaa in position 13 is omitted
Xaa in position 14 is Ala, Ser, Asn, Val or Pro
Xaa in position 15 is Ile, Leu, Met or Val,
Xaa in position 16 is Ser or Thr
Xaa in position 17 is Pro or Ala,
Xaa in position 18 is Arg or Lys,
Xaa in position 19 is Thr or Ser
Xaa in position 20 is Leu or Ser
Xaa in position 21 is Asn, Phe or Val,
Xaa in position 23 is Trp, Tyr, Gly or none
Xaa in position 24 is Val, Leu, Gly or none
Xaa in position 25 is Lys, Arg, Gly or none
Xaa in position 26 is Val, Ala, Cys, Gly or none
wherein the sequence of SEQ ID NO : 4 comprises at least six consecutive amino acids and –Z- is optional and have the meaning PEG, modified PEG and/or $[Gly]_n$, wherein n = 1,2 or 3,

Xaa_1 Ala Xaa_3 Xaa_4 Xaa_5 Ala Xaa_7 Xaa_8 Xaa_9 Leu Leu Xaa_{12} Xaa_{13} Xaa_{14} –Z- Xaa_{15} Xaa_{16} His Gln Xaa_{19} Ala Xaa_{21} Xaa_{22} (SEQ ID NO : 9)

wherein Xaa in position 1 is Tyr, Trp, Phe or Gly
Xaa in position 3 is Thr, Ala, Val, Ile or Leu
Xaa in position 4 is Pro or Ser
Xaa in position 5 is Gln, His, Gly, Thr, Ser or Tyr
Xaa in position 7 is Leu, Ile or Val
Xaa in position 8 is Asn or Tyr
Xaa in position 9 is Thr, Met, Leu or Ala

Xaa in position 12 is Ser, Thr or Asn
Xaa in position 13 is Thr, Ile, Val or Ala
Xaa in position 14 is Val or Ile
Xaa in position 15 is Gly or none
Xaa in position 16 is Gly or none
Xaa in position 19 is Ala or Gly
Xaa in position 20 is Ala
Xaa in position 21 is Met, Leu, Cys or none
Xaa in position 22 is Gln, Glu, His, Gly or none
wherein the sequence of SEQ ID NO : 9 consists of at least six consecutive amino acids and the linker –Z- is optional and have the meaning PEG, modified PEG and/or $[Gly]_n$, wherein n = 1,2 or 3,

$Xaa_1\ Xaa_2$ Ala Leu Ala Gly $Xaa_7\ Xaa_8\ Xaa_9$ Leu $Xaa_{11}\ Xaa_{12}\ Xaa_{13}\ Xaa_{14}\ Xaa_{15}\ Xaa_{16}$ $Xaa_{17}\ Xaa_{18}\ Xaa_{19}\ Xaa_{20}\ Xaa_{21}$ (SEQ ID NO : 15)

wherein the Xaa in position 1 is Trp or Tyr
Xaa in position 2 is Ser or Ala
Xaa in position 7 is Thr, Ala or Ser
Xaa in position 8 is Ser or Thr
Xaa in position 9 is Ser or Thr
Xaa in position 11 is Leu, Pro, Val or Gln
Xaa in position 12 is Gln, Ala or His
Xaa in position 13 is Glu or Gly
Xaa in position 14 is Gln or His
Xaa in position 15 is Ile, Leu, Val or Met
Xaa in position 16 is Gly, Ala, Gln, Thr, Asn, Arg, His or Ile
Xaa in position 17 is Trp or Tyr
Xaa in position 18 is Thr, Met, Leu or Ile
Xaa in position 19 is Thr or Ser
Xaa in position 20 is Cys, Gly or none
Xaa in position 21 is Gly or none
wherein the sequence of SEQ ID NO : 15 consists of at least six consecutive amino acids,

the terminal ends of the sequences may be free carboxyl- or amino groups, amides, acyls, acetyls or salts thereof,
two or more of the Cys residues may form part of an interchain disulphide binding, a -S-$(CH_2)_p$-S- or a - $(CH_2)_p$-bridge wherein p = 1-8 optionally intervened by one or more hetero atoms such as O, N and S and/or the said peptide sequences are immobilized to a solid support.

2. Peptide according to claim 1, characterized in that
the amino acid sequence of SEQ ID NO : 1 is selected from the groups of SEQ ID NO : 2 and SEQ ID NO : 3.

3. Peptide according to claim 1, characterized in that
the amino acid sequence of SEQ ID NO : 4 is selected from the groups of SEQ ID NO : 5, SEQ ID NO : 6 and SEQ ID NO : 8.

4. Peptide according to claim 1, characterized in that
the amino acid sequence of SEQ ID NO : 9 is selected from the groups of SEQ ID NO : 11 and SEQ ID NO : 12.

5. Peptide according to claim 1, characterized in that
the amino acid sequence of SEQ ID NO : 15 is SEQ ID NO : 14.

6. Antigen, characterized in that it comprises at least one peptide according to claim 1.

7. Antigen according to claim 6, characterized in that it comprises at least one peptide selected from at least one of the groups SEQ ID NO : 1, SEQ ID NO : 4, SEQ ID NO : 9 and SEQ ID NO : 15.

8. Vaccine composition, characterized in that
it comprises an antigen according to claim 6 with a pharmaceutically acceptable diluent and optionally an adjuvant, carrier and/or vehicle and optionally additional immunostimulatory compound(s).

9. Vaccine composition according to claim 8, characterized in that it comprises at least one peptide selected from the groups of SEQ ID NO : 1, SEQ ID NO : 4, SEQ ID NO : 9 and SEQ ID NO : 15.

10. Vaccine composition according to claim 8, characterized in that it comprises the peptides of the SEQ ID NO : 3, SEQ ID NO : 6, SEQ ID NO : 11 and SEQ ID NO : 14.

11. Vaccine composition according to the claims 8-10 characterized in that the peptides are dissolved in a sterile water solution and the optional immunostimulatory compound is a granulocyte macrophage colony stimulating factor.

12. Vaccine composition according to the claims 8-11 characterized in that the composition comprises an adjuvant selected from the group Monophosphoryl Lipid A (MPL®), Freund`s complete or incomplete adjuvant or aluminum hydroxyd.

13. Vaccine composition, characterized in that an antigen according to claim 6 is formulated as a lipopeptide and/or a liposome formulation.

14. A method of detecting antibodies, induced by a HIV or HIV-specific peptide(s) or protein(s), in a sample of body fluid characterized in that subjecting the said sample to an immunoassay, wherein the antigen(s) is/are selected from the peptides of the claims 1, 2, 3 , 4 and 5.

15. An immunoassay kit for the detection of antibodies, induced by a HIV or HIV-specific peptides or proteins, in a sample of body fluid, characterized in that the diagnostic antigen is a peptide of any one of the previous claims 1 to 5.

16. Antibody, characterized in that it is capable of selectively reacting with the antigen of the claims 6 and 7.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
(A) NAME: Bionor Immuno AS
(B) STREET: Strømdalsjordet 4, P.O.Box 1893 Gulset
(C) CITY: 3703 Skien
(E) COUNTRY: Norway
(F) POSTAL CODE (ZIP): N-3705
(G) TELEPHONE: +47 35 50 57 50
(H) TELEFAX: + 47 35 50 57 01

(i) INVENTOR:
(A) NAME : Birger Sørensen
(B) STREET : Meierlia 3
(C) CITY : 3727 Skien
(D) COUNTRY : Norway

(ii) TITLE OF INVENTION: HIV peptides, antigens, vaccine compositions, immunoassay and a method of detecting antibodies induced by HIV.

(iii) NUMBER OF SEQUENCES: 17

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: Windows 2000
(D) SOFTWARE: Word 7.0

(v) CURRENT APPLICATION DATA:
APPLICATION NUMBER:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: No

(v) FRAGMENT TYPE : internal

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1

(D) OTHER INFORMATION: /note= " Xaa in position 1 is His, Lys or Arg

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /note= " Xaa in position 2 is Ile, Leu, Val or Met

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(D) OTHER INFORMATION: /note= " Xaa in position 3 is Ile or Val

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 4
(D) OTHER INFORMATION: /note= " Xaa in position 4 is Trp or Tyr

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /note= " Xaa in position 5 is Ala or Leu

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 6
(D) OTHER INFORMATION: /note= " Xaa in position 6 is Ser, Thr, Arg or Asn

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 7
(D) OTHER INFORMATION: /note= " Xaa in position 7 is Arg or Ser

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(A) NAME/KEY: Modified-site
(B) LOCATION: 11
(D) OTHER INFORMATION: /note= " Xaa in position 11 is Arg, Lys, Gly, or Asn

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 12
(D) OTHER INFORMATION: /note= " Xaa in position 12 is Phe, Ser or Tyr

ix) FEATURE:
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(B) LOCATION: 13
(D) OTHER INFORMATION: /note= " Xaa in position 13 is Ala, Thr or Ser

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 14
(D) OTHER INFORMATION: /note= " Xaa in position 14 is Val, Leu, Ile or Cys

ix) FEATURE:
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(B) LOCATION: 15

(D) OTHER INFORMATION: /note= " Xaa in position 15 is Asn, Ser or Asp

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 16
(D) OTHER INFORMATION: /note= " Xaa in position 16 is Pro, Arg or Ser

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 17
(D) OTHER INFORMATION: /note= " Xaa in position 17 is Gly, Ser, Ala, Asp or Asn

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 18
(D) OTHER INFORMATION: /note= " Xaa in position 18 is Leu or Phe

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 19
(D) OTHER INFORMATION: /note= " Xaa in position 19 is Leu or Met

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 20
(D) OTHER INFORMATION: /note= " Xaa in position 20 is Glu, Gly, Asp or Ile

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 21
(D) OTHER INFORMATION: /note= " Xaa in position 21 is Thr, Ser or Ala

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

$Xaa_1\ Xaa_2\ Xaa_3\ Xaa_4\ Xaa_5\ Xaa_6\ Xaa_7$ Gln Leu Gln $Xaa_{11}Xaa_{12}\ Xaa_{13}Xaa_{14}\ Xaa_{15}\ Xaa_{16}$
1 5 10 15

$Xaa_{17}Xaa_{18}\ Xaa_{19}\ Xaa_{20}Xaa_{21}$
20

(2) INFORMATION FOR SEQ ID NO:2:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

His Leu Ile Tyr Leu Thr Arg Gln Leu Gln Arg Phe Ala Leu Asn Pro Gly Leu Leu Ile Thr

1 5 10 15 20

(2) INFORMATION FOR SEQ ID NO:3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Arg Leu Ile Tyr Ala Thr Arg Gln Leu Gln Arg Phe Ala Val Asn Pro Gly Leu Leu Ile Thr
1 5 10 15 20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: No
(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= " Xaa in position 1 is Pro, Tyr or Phe

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /note= " Xaa in position 2 is Ile, Val or Leu

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(D) OTHER INFORMATION: /note= " Xaa in position 3 is Ile, Leu, Val, Ala or Met

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 4
(D) OTHER INFORMATION: /note= " Xaa in position 4 is Gln, Ser, Thr or Val

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /note= " Xaa in position 5 is Asn, Asp or Thr

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 6

(D) OTHER INFORMATION: /note= " Xaa in position 6 is Ile, Ala, Leu or Met

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 7
(D) OTHER INFORMATION: /note= " Xaa in position 7 is Gln, Glu, Lys or Gly

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 9
(D) OTHER INFORMATION: /note= " Xaa in position 9 is Gln or Ile

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 13
(D) OTHER INFORMATION: /note= " Xaa in position 13 is removed

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 14
(D) OTHER INFORMATION: /note= " Xaa in position 14 is Ala, Ser, Asn, Val or Pro

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 15
(D) OTHER INFORMATION: /note= " Xaa in position 15 is Ile, Leu, Met or Val

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 16
(D) OTHER INFORMATION: /note= " Xaa in position 16 is Ser or Thr

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 17
(D) OTHER INFORMATION: /note= " Xaa in position 17 is Pro or Ala

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 18
(D) OTHER INFORMATION: /note= " Xaa in position 18 is Arg or Lys

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 19
(D) OTHER INFORMATION: /note= " Xaa in position 19 is Thr or Ser

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 20
(D) OTHER INFORMATION: /note= " Xaa in position 20 is Leu or Ser

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 21
(D) OTHER INFORMATION: /note= " Xaa in position 21 is Asn, Phe or Val

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 23
(D) OTHER INFORMATION: /note= " Xaa in position 23 is Trp, Tyr, Gly or none

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 24
(D) OTHER INFORMATION: /note= " Xaa in position 24 is Val, Leu, Gly or none

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 25
(D) OTHER INFORMATION: /note= " Xaa in position 25 is Lys, Arg, Gly or none

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 26
(D) OTHER INFORMATION: /note= " Xaa in position 26 is Val, Ala, Cys, Gly or none

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 11..12
(D) OTHER INFORMATION: /note= " optionally inserted a -Z- linker which is PEG, modified PEG and/or $[Gly]_n$ wherein n = 1, 2 or 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

$Xaa_1\ Xaa_2\ Xaa_3\ Xaa_4\ Xaa_5\ Xaa_6\ Xaa_7$ Gly Xaa_9 Leu Val –Z-Tyr $Xaa_{14}Xaa_{15}\ Xaa_{16}$
1 5 10 15
$Xaa_{17}\ Xaa_{18}\ Xaa_{19}\ Xaa_{20}\ Xaa_{21}$ Ala $Xaa_{23}\ Xaa_{24}\ Xaa_{25}\ Xaa_{26}$
20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Tyr Ile Leu Gln Asn Ile Glu Gly Gln Leu Val Gly Gly Gly Tyr Ala Ile Ser Pro Arg Thr Leu
1 5 10 15 20
Val Ala Tyr Leu Arg Gly-NH_2
25

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: No
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Phe Ile Leu Gln Asn Ile Glu Gly Gln Leu Val Gly Gly Gly Tyr Ala Ile Ser Pro Arg Thr Leu
1 5 10 15 20

Val Ala Gly Gly Gly Gly -OH
25

(2) INFORMATION FOR SEQ ID NO:7:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: No, nativ p24 sequence
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Pro Ile Val Gln Asn Ile Glu Gly Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala
1 5 10 15 20

Trp Val Lys Val
25

(2) INFORMATION FOR SEQ ID NO: 8

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

Phe Ile Leu Gln Asn Ile Gln Gly Gln Leu Val Gly Gly Gly Tyr Ala Ile Ser Pro Arg Thr Leu
1 5 10 15 20
Val Ala Gly
25

(2) INFORMATION FOR SEQ ID NO: 9

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: No

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= " Xaa in position 1 is Tyr, Trp, Phe or Gly

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(D) OTHER INFORMATION: /note= " Xaa in position 3 is Thr, Ala, Val, Ile or Leu

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 4
(D) OTHER INFORMATION: /note= " Xaa in position 4 is Pro or Ser

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /note= " Xaa in position 5 is Gln, His, Gly, Thr, Ser or Tyr

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 7
(D) OTHER INFORMATION: /note= " Xaa in position 7 is Leu, Ile or Val

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 8
(D) OTHER INFORMATION: /note= " Xaa in position 8 is Asn or Tyr

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 9
(D) OTHER INFORMATION: /note= " Xaa in position 9 is Thr, Met, Leu or Ala

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 12
(D) OTHER INFORMATION: /note= " Xaa in position 12 is Ser, Thr or Asn

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 13
(D) OTHER INFORMATION: /note= " Xaa in position 13 is Thr, Ile, Val or Ala

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 14
(D) OTHER INFORMATION: /note= " Xaa in position 14 is Val or Ile

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 15
(D) OTHER INFORMATION: /note= " Xaa in position 15 is Gly or none

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 16
(D) OTHER INFORMATION: /note= " Xaa in position 16 is Gly or none

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 19
(D) OTHER INFORMATION: /note= " Xaa in position 19 is Ala or Gly

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 21
(D) OTHER INFORMATION: /note= " Xaa in position 21 is Met, Leu, Cys or none

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 22
(D) OTHER INFORMATION: /note= " Xaa in position 22 is Gln, Glu, His, Gly or none

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 14..15
(D) OTHER INFORMATION: /note= " optionally inserted linker –Z- which is PEG, modified PEG and/or $[Gly]_n$ wherein n = 1, 2 or 3

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 21
(D) OTHER INFORMATION: /note= " Cys in position 21 may form part of a disulphide-bond

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

Xaa_1 Ala Xaa_3 Xaa_4 Xaa_5 Ala Xaa_7 Xaa_8 Xaa_9 Leu Leu Xaa_{12} Xaa_{13} Xaa_{14} –Z- Xaa_{15}
1 5 10 15
Xaa_{16} His Gln Xaa_{19} Ala Xaa_{21} Xaa_{22}
20

(2) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: No, nativ p24 sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln Ala Ala
1 5 10 15 20

(2) INFORMATION FOR SEQ ID NO: 11

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

Tyr Ala Ile Pro Gln Ala Leu Asn Thr Leu Leu Asn Thr Val Gly Gly His Gln Ala Ala
1 5 10 15 20

(2) INFORMATION FOR SEQ ID NO:12

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: No

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 23
(D) OTHER INFORMATION: /note= " Cys in position 23 may form part of a disulphide-bond

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

Phe Ala Ile Pro Gln Ala Leu Asn Thr Leu Leu Asn Thr Val Gly Gly Gly Gly His Gln Ala
1 5 10 15 20
Ala Cys Gly

2) INFORMATION FOR SEQ ID NO:13

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: No, nativ p24 sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:14

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

Trp Ser Ala Leu Ala Gly Thr Thr Ser Leu Leu Gln Gly Gln Leu Gly Trp Ile Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: both
(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: No

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= " Xaa in position 1 is Trp, Tyr

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /note= " Xaa in position 2 is Ser or Ala

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 7
(D) OTHER INFORMATION: /note= " Xaa in position 7 is Thr, Ala or Ser

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 8
(D) OTHER INFORMATION: /note= " Xaa in position 8 is Ser or Thr

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 9
(D) OTHER INFORMATION: /note= " Xaa in position 9 is Ser or Thr

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 11
(D) OTHER INFORMATION: /note= " Xaa in position 11 is Leu, Pro, Val or Gln

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 12
(D) OTHER INFORMATION: /note= " Xaa in position 12 is Gln, Ala or His

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 13
(D) OTHER INFORMATION: /note= " Xaa in position 13 is Gly or Glu

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 14
(D) OTHER INFORMATION: /note= " Xaa in position 14 is Gln or His

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 15
(D) OTHER INFORMATION: /note= " Xaa in position 15 is Ile, Leu, Val or Met

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 16
(D) OTHER INFORMATION: /note= " Xaa in position 16 is Gly, Ala, Gln, Thr, Asn, Arg, His or Ile

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 17
(D) OTHER INFORMATION: /note= " Xaa in position 17 is Trp ot Tyr

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 18
(D) OTHER INFORMATION: /note= " Xaa in position 18 is Thr, Ile, Leu or Met

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 19
(D) OTHER INFORMATION: /note= " Xaa in position 19 is Thr or Ser

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 20
(D) OTHER INFORMATION: /note= " Xaa in position 20 is Cys, Gly or none

ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 21
(D) OTHER INFORMATION: /note= " Xaa in position 21 is Gly or none

ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 20
(D) OTHER INFORMATION: /note= " Cys in position 20 may form part of a disulphide-bond

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

Xaa_1 Xaa_2 Ala Leu Ala Gly Xaa_7 Xaa_8 Xaa_9 Leu Xaa_{11} Xaa_{12} Xaa_{13} Xaa_{14} Xaa_{15}
1 5 10 15
Xaa_{16} Xaa_{17} Xaa_{18} Xaa_{19} Xaa_{20} Xaa_{21}
20

2) INFORMATION FOR SEQ ID NO:16

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: No, nativ p17 sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro Gly Leu Leu Glu Thr
1 5 10 15 20

2) INFORMATION FOR SEQ ID NO:17

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: No, nativ p24 sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17

Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp
1 5 10 15 20

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
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(71) Applicant *(for all designated States except US)*: **BIONOR IMMUNO AS** [NO/NO]; Strömdalsjordet 4, N-3703 Skien (NO).

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(75) Inventor/Applicant *(for US only)*: **SÖRENSEN, Birger** [NO/NO]; Meierlia 3, N-3727 Skien (NO).

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(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

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Published:
— *with international search report*
— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments*

(88) Date of publication of the international search report:
13 June 2002

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 02/20554 A3

(54) Title: HIV PEPTIDES FROM CONSERVED REGIONS IN GAG P17 AND 924 AND THEIR APPLICATION IN E.G. VACCINES

(57) Abstract: The present invention comprises novel and modified peptides capable of inducing a HIV-1 specific immune response without antagonizing the cytotoxic T-cell activity in order to achieve an effective prophylactic and therapeutic vaccine against HIV. The peptides are based on conserved regions of HIV gag p17 and p24 proteins. Antigens in free- or carrier-bound form comprising at least one of the said peptides, vaccine compositions containing at least one of the antigens, immunoassay kits and a method of detecting antibodies induced by HIV or HIV specific peptides using such antigens, are described.

PATENT COOPERATION TREATY

PCT

INTERNATIONAL SEARCH REPORT

(PCT Article 18 and Rules 43 and 44)

Applicant's or agent's file reference 104826/HNY	FOR FURTHER ACTION	see Notification of Transmittal of International Search Report (Form PCT/ISA/220) as well as, where applicable, item 5 below.
International application No. PCT/NO 01/00362	International filing date *(day/month/year)* 3 Sept 2001	(Earliest) Priority Date *(day/month/year)* 4 Sept 2000
Applicant Bionor Immuno AS et al		

This international search report has been prepared by this International Searching Authority and is transmitted to the applicant according to Article 18. A copy is being transmitted to the International Bureau.

This international search report consists of a total of 6 sheets.

[X] It is also accompanied by a copy of each prior art document cited in this report.

1. **Basis of the report**

a. With regard to the language, the international search was carried out on the basis of the international application in the language in which it was filed, unless otherwise indicated under this item.

[ ] the international search was carried out on the basis of a translation of the international application furnished to this Authority (Rule 23.1(b)).

b. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of the sequence listing:

[X] contained in the international application in written form.

[X] filed together with the international application in computer readable form.

[ ] furnished subsequently to this Authority in written form.

[ ] furnished subsequently to this Authority in computer readable form.

[ ] the statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.

[ ] the statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished.

2. [ ] Certain claims were found unsearchable (See Box I).

3. [X] Unity of invention is lacking (See Box II).

4. With regard to the title,

[ ] the text is approved as submitted by the applicant.

[X] the text has been established by this Authority to read as follows:

HIV PEPTIDES FROM CONSERVED REGIONS IN GAG P17 AND P24 AND THEIR APPLICATION IN E.G. VACCINES.

5. With regard to the abstract,

[X] the text is approved as submitted by the applicant.

[ ] the text has been established, according to Rule 38.2(b), by this Authority as it appears in Box III. The applicant may, within one month from the date of mailing of this international search report, submit comments to this Authority.

6. The figure of the drawings to be published with the abstract is Figure No. -

[ ] as suggested by the applicant.

[ ] because the applicant failed to suggest a figure.

[ ] because this figure better characterizes the invention.

[ ] None of the figures.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/NO 01/00362

A. CLASSIFICATION OF SUBJECT MATTER

IPC7: C07K 14/16, A61K 39/21, G01N 33/569
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC7: C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

SE,DK,FI,NO classes as above

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-INTERNAL, BIOSIS, EBI

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GB 2236754 A (VIRAL TECHNOLOGIES INC), 17 April 1991 (17.04.91), pages 7-11 (peptide B, HGP18, HGP18(2)), page 20, example 1, claim 9	1,2,6-9, 11-16
A		10
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X	WO 9837089 A2 (OXFORD BIOMEDICA (UK) LIMITED), 27 August 1998 (27.08.98), claims, pages 4, 8, 15-19	1,2,6-9, 11-16
A		10
	--	

[X] Further documents are listed in the continuation of Box C. [X] See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
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"X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
2 April 2002	04-04-2002
Name and mailing address of the ISA/ Swedish Patent Office Box 5055, S-102 42 STOCKHOLM Facsimile No. +46 8 666 02 86	Authorized officer Carl-Olof Gustafsson/BS Telephone No. +46 8 782 25 00

INTERNATIONAL SEARCH REPORT

International application No.
PCT/NO 01/00362

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EP 0732339 A1 (BEHRINGWERKE AKTIENGESELLSCHAFT), 18 Sept 1996 (18.09.96), page 2, page 6	1,2,6-9, 11-16
A	--	10
A	WO 9958658 A2 (EPIMMUNE, INC.), 18 November 1999 (18.11.99), pages 70-73, 16-27	
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INTERNATIONAL SEARCH REPORT

Information on patent family members

28/01/02

International application No.
PCT/NO 01/00362

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		SE 0426314 T3	
		EP 0620009 A	19/10/94
		EP 0620010 A	19/10/94
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		NZ 235538 A	25/06/92
		ZA 9007944 A	30/10/91
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		GB 9703802 D	00/00/00
		GB 9918843 D	00/00/00
		JP 2001512323 T	21/08/01
		US 6287572 B	11/09/01
EP 0732339 A1	18/09/96	AT 143974 T	15/10/96
		AU 661464 B	27/07/95
		AU 8976691 A	18/06/92
		CA 2057612 A	15/06/92
		DE 4039925 A	17/06/92
		DE 59108261 D	00/00/00
		DK 490383 T	17/02/97
		EP 0490383 A,B	17/06/92
		SE 0490383 T3	
		ES 2095899 T	01/03/97
		IE 914353 A	17/06/92
		JP 6107697 A	19/04/94
		PT 99791 A,B	31/12/92
		US 5612453 A	18/03/97
WO 9958658 A2	18/11/99	AU 4078599 A	29/11/99
		EP 1078092 A	28/02/01
		US 6018862 A	01/02/00
		US 6301076 B	09/10/01

INTERNATIONAL SEARCH REPORT

International application No.
PCT/NO01/00362

Box I **Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II **Observations where unity of invention is lacking (Continuation of item 2 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

see next sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

According to PCT Rule 13.2, an international application shall relate to one invention only or a group of inventions linked by one or more of the same or corresponding "special technical features", i.e. features that define a contribution which each of the inventions makes over the prior art.

The claimed invention relates to HIV peptides and their application in vaccines, assays etc.. Four groups of peptides from HIV Gag are claimed. However such groups of peptides from HIV Gag are known in the art and have been used for the improvement of vaccines and assays, see e.g. GB2236754, pages 7-11. Therefore the application fails, a posteriori, to comply with PCT-rule 13.2.

The following inventions have been found:

Invention 1. Claims: 1, 2, 6-16 partially.
Peptides, vaccines, antibodies etc. selected from Gag residues 33-53 with "conserved" amino acids ..QLQ.. and corresponding antigen and vaccines. SEQ IDs 1-3, 14 and 16.

Invention 2. Claims: 1, 3, 6-9, 11-16 partially.
Peptides, vaccines, antibodies etc. selected from Gag residues 133-157 with "conserved" amino acids P..GQXXHQXXXXRT...K and corresponding antigen and vaccines. SEQ IDs 4-8 and 17.

Invention 3. Claims: 1, 4, 6-9, 11-16 partially
Peptides, vaccines, antibodies etc. selected from Gag residues 178-198 with "conserved" amino acids GA..D...MLGXHQXAX and corresponding antigen and vaccines. SEQ IDs 9-12

Invention 4. Claims: 1, 5, 6-9, 11-16 (partially).
Peptides, vaccines, antibodies etc. selected from Gag residues 233-251 with "conserved" amino acids GXXXAG.....EXXXWXX and corresponding antigen and vaccines. SEQ IDs 13-15

Invention 5. Claims: 1, 10
Combinations of peptides in e.g. vaccines, diagnostics according to claim 10 and to claims 1-9 and 11-16 partially. Only one example of a selected combination is revealed in the description and consequently no search for other combinations than the one given in claim 10 is feasible.

../..

Each peptide in claim 1 is defined by a few "conserved" amino acids (aa) only and the rest of the peptide is variable. Support for the variable amino acids are not found in the examples although most (all?) are known as conserved aa in HIV. Consequently the present search has been focused on the general aspects of the SEQ ID NO 1 peptides in claim 1 and corresponding vaccine or assay applications and to the selected peptides according to the corresponding examples.

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

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Published:
— *with international search report*
— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments*

(88) Date of publication of the international search report:
13 June 2002

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 02/20554 A3

(54) Title: HIV PEPTIDES FROM CONSERVED REGIONS IN GAG P17 AND 924 AND THEIR APPLICATION IN E.G. VACCINES

(57) Abstract: The present invention comprises novel and modified peptides capable of inducing a HIV-1 specific immune response without antagonizing the cytotoxic T-cell activity in order to achieve an effective prophylactic and therapeutic vaccine against HIV. The peptides are based on conserved regions of HIV gag p17 and p24 proteins. Antigens in free- or carrier-bound form comprising at least one of the said peptides, vaccine compositions containing at least one of the antigens, immunoassay kits and a method of detecting antibodies induced by HIV or HIV specific peptides using such antigens, are described.

PATENT COOPERATION TREATY

PCT

INTERNATIONAL SEARCH REPORT

(PCT Article 18 and Rules 43 and 44)

Applicant's or agent's file reference	FOR FURTHER ACTION	see Notification of Transmittal of International Search Report (Form PCT/ISA/220) as well as, where applicable, item 5 below.
104826/HNY		
International application No.	International filing date *(day/month/year)*	(Earliest) Priority Date *(day/month/year)*
PCT/NO 01/00362	3 Sept 2001	4 Sept 2000
Applicant		
Bionor Immuno AS et al		

This international search report has been prepared by this International Searching Authority and is transmitted to the applicant according to Article 18. A copy is being transmitted to the International Bureau.

This international search report consists of a total of 6 sheets.

[X] It is also accompanied by a copy of each prior art document cited in this report.

1. **Basis of the report**

   a. With regard to the language, the international search was carried out on the basis of the international application in the language in which it was filed, unless otherwise indicated under this item.

   [ ] the international search was carried out on the basis of a translation of the international application furnished to this Authority (Rule 23.1(b)).

   b. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of the sequence listing:

   [X] contained in the international application in written form.

   [X] filed together with the international application in computer readable form.

   [ ] furnished subsequently to this Authority in written form.

   [ ] furnished subsequently to this Authority in computer readable form.

   [ ] the statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.

   [ ] the statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished.

2. [ ] Certain claims were found unsearchable (See Box I).

3. [X] Unity of invention is lacking (See Box II).

4. With regard to the title,

   [ ] the text is approved as submitted by the applicant.

   [X] the text has been established by this Authority to read as follows:

   HIV PEPTIDES FROM CONSERVED REGIONS IN GAG P17 AND P24 AND THEIR APPLICATION IN E.G. VACCINES.

5. With regard to the abstract,

   [X] the text is approved as submitted by the applicant.

   [ ] the text has been established, according to Rule 38.2(b), by this Authority as it appears in Box III. The applicant may, within one month from the date of mailing of this international search report, submit comments to this Authority.

6. The figure of the drawings to be published with the abstract is Figure No. -

   [ ] as suggested by the applicant.

   [ ] because the applicant failed to suggest a figure.

   [ ] because this figure better characterizes the invention.

   [ ] None of the figures.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/NO 01/00362

A. CLASSIFICATION OF SUBJECT MATTER

IPC7: C07K 14/16, A61K 39/21, G01N 33/569
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC7: C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

SE,DK,FI,NO classes as above

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-INTERNAL, BIOSIS, EBI

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GB 2236754 A (VIRAL TECHNOLOGIES INC), 17 April 1991 (17.04.91), pages 7-11 (peptide B, HGP18, HGP18(2)), page 20, example 1, claim 9	1,2,6-9, 11-16
A	--	10
X	WO 9837089 A2 (OXFORD BIOMEDICA (UK) LIMITED), 27 August 1998 (27.08.98), claims, pages 4, 8, 15-19	1,2,6-9, 11-16
A	--	10

[X] Further documents are listed in the continuation of Box C. [X] See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
2 April 2002	04-04-2002
Name and mailing address of the ISA/ Swedish Patent Office Box 5055, S-102 42 STOCKHOLM Facsimile No. +46 8 666 02 86	Authorized officer Carl-Olof Gustafsson/BS Telephone No. +46 8 782 25 00

INTERNATIONAL SEARCH REPORT

International application No.
PCT/NO 01/00362

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EP 0732339 A1 (BEHRINGWERKE AKTIENGESELLSCHAFT), 18 Sept 1996 (18.09.96), page 2, page 6	1,2,6-9, 11-16
A	--	10
A	WO 9958658 A2 (EPIMMUNE, INC.), 18 November 1999 (18.11.99), pages 70-73, 16-27	
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INTERNATIONAL SEARCH REPORT

Information on patent family members

28/01/02

International application No.
PCT/NO 01/00362

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
GB 2236754 A	17/04/91	AT 119166 T	15/03/95
		AU 6393990 A	18/04/91
		CA 2027455 A	13/04/91
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		DE 69017352 D,T	05/10/95
		DK 426314 T	27/03/95
		EP 0426314 A,B	08/05/91
		SE 0426314 T3	
		EP 0620009 A	19/10/94
		EP 0620010 A	19/10/94
		ES 2071038 T	16/06/95
		GB 9021942 D	00/00/00
		GR 3015244 T	30/06/95
		HU 55035 A	29/04/91
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WO 9958658 A2	18/11/99	AU 4078599 A	29/11/99
		EP 1078092 A	28/02/01
		US 6018862 A	01/02/00
		US 6301076 B	09/10/01

INTERNATIONAL SEARCH REPORT

International application No.
PCT/NO01/00362

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see next sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

According to PCT Rule 13.2, an international application shall relate to one invention only or a group of inventions linked by one or more of the same or corresponding "special technical features", i.e. features that define a contribution which each of the inventions makes over the prior art.

The claimed invention relates to HIV peptides and their application in vaccines, assays etc.. Four groups of peptides from HIV Gag are claimed. However such groups of peptides from HIV Gag are known in the art and have been used for the improvement of vaccines and assays, see e.g. GB2236754, pages 7-11. Therefore the application fails, a posteriori, to comply with PCT-rule 13.2.

The following inventions have been found:

Invention 1. Claims: 1, 2, 6-16 partially.
Peptides, vaccines, antibodies etc. selected from Gag residues 33-53 with "conserved" amino acids ..QLQ.. and corresponding antigen and vaccines. SEQ IDs 1-3, 14 and 16.

Invention 2. Claims: 1, 3, 6-9, 11-16 partially.
Peptides, vaccines, antibodies etc. selected from Gag residues 133-157 with "conserved" amino acids P..GQXXHQXXXXRT...K and corresponding antigen and vaccines. SEQ IDs 4-8 and 17.

Invention 3. Claims: 1, 4, 6-9, 11-16 partially
Peptides, vaccines, antibodies etc. selected from Gag residues 178-198 with "conserved" amino acids GA..D..MLGXHQXAX and corresponding antigen and vaccines. SEQ IDs 9-12

Invention 4. Claims: 1, 5, 6-9, 11-16 (partially).
Peptides, vaccines, antibodies etc. selected from Gag residues 233-251 with "conserved" amino acids GXXXAG....EXXXWXX and corresponding antigen and vaccines. SEQ IDs 13-15

Invention 5. Claims: 1, 10
Combinations of peptides in e.g. vaccines, diagnostics according to claim 10 and to claims 1-9 and 11-16 partially. Only one example of a selected combination is revealed in the description and consequently no search for other combinations than the one given in claim 10 is feasible.

../..

Each peptide in claim 1 is defined by a few "conserved" amino acids (aa) only and the rest of the peptide is variable. Support for the variable amino acids are not found in the examples although most (all?) are known as conserved aa in HIV. Consequently the present search has been focused on the general aspects of the SEQ ID NO 1 peptides in claim 1 and corresponding vaccine or assay applications and to the selected peptides according to the corresponding examples.